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A scenario of co-evolution between badnaviruses and *Musa sp.*

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The banana streak disease is due to a complex of distinct Banana streak viruses (BSVs) species showing a wide genetic diversity. Banana streak viruses (BSVs) are double stranded DNA pararetroviruses belonging to the family *Caulimoviridae*, genus Badnavirus. Outbreaks of BSVs causing banana streak disease have been recorded worldwide where *Musa* spp. is grown during the last 20 years with no convincing evidence of epidemics. Epidemics were previously reported in Uganda where BSV is currently endemic. In addition, the banana genome (*Musa* sp.) is invaded by numerous badnavirus sequences. The majority of these viral integrants is mostly defective as a result of pseudogenisation driven by the host genome evolution. They are just called BEV (banana endogenous virus sequences) because episomal particles corresponding to the integrated counterparts have not been identified so far. Conversely, only few viral integrants named endogenous BSV (eBSVs) can release a functional BSV genome following stresses. All the badnaviral sequences described so far are spread among the three main clades of the badnavirus genus diversity.
Our group established that BSVs are distributed among Clade I and Clade III. Clade I gathers BSV species distributed worldwide whereas Clade III is dedicated to BSV species only present in Uganda. eBSVs exclusively correspond to BSV species of Clade I and are endogenous to the *Musa balbisiana* (B) genomes only. We elucidated their sequence and organization for three BSV species (BSOLV, BSGFV and BSIMV) present in the seedy banana diploid PKW (BB). In addition, we established that all BEVs sequences belong to Clade II. All together our results allowed us to propose an evolutionary scheme of badnavirus and banana co-evolution, which is presented here.

Mots-clés : Badnavirus diversity, *Banana streak virus BSV*, endogenous *Banana streak virus*, *Musa*, *M. acuminata, Musa balbisiana.*